

#6

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/809,638

DATE: 08/08/2001
TIME: 11:01:34

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\08082001\I809638.raw

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4 <110> APPLICANT: Mary Faris
5   Pia M. Challita-Eid
6   Steve Chappell Mitchell
7   Daniel E.H. Afar
8   Arthur B. Raitano
9   Aya Jakobovits
11 <120> TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN
12   HIGHLY EXPRESSED IN VARIOUS CANCERS
15 <130> FILE REFERENCE: 129.35US01
17 <140> CURRENT APPLICATION NUMBER: 09/809,638
18 <141> CURRENT FILING DATE: 2001-03-14
20 <160> NUMBER OF SEQ ID NOS: 746
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2103
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1

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32 gggcttaag gttagtat agcatttctt tctcaataat tcctaacaat tactccccc	180
33 tggaaattgg ttaacaagaa gtggatgcta accctgctga ggataatcac tattggcage	240
34 atagcctcct tccaggctcc aaatgcacaa cttcgactga tggttcttgc gcttgggtg	300
35 tctcctcac tgatagtgc agctgtgact tgggtgtcgg gaagtcatgg ccaaaggta	360
36 ctcagaattt gggattcat tttaggacag attgttcttgc ttgttctacg catatggat	420
37 acttcactaa acccaatctg gagttatcag atgtccaaca aagtataact gacattaagt	480
38 gccatagcca cacttgc tattggcaca gatggact gcaatggaa tgaagaaaag	540
39 aagactggtg agtagccac gggatggcc tctagacccaa actggctgct ggcaggggct	600
40 gctttggta gccttgc tccacccac tgggttttg gagaagtctc tcttggcc	660
41 agatgggcag tgagtggca tccacatcca gggccagatc ctaacccatt tggaggtgca	720
42 gtaatgtgt gcttggcaag tgattgtat cttccatctt gtttgggtt tcgtgtact	780
43 ggtttgatct ggtgggtac agaacagct tcagctgccc gctccctta cctgcacaca	840
44 tggcagctg ctgtgtctgg ctgtgtcttc gccatctta ctgcatccat gtggcccaa	900
45 acacttggac accttattaa ctcaggacaa aaccctggaa aaaccatgac catggccat	960
46 atattttata ttctagaaat attttctgt gcctggcata cagttttaa gtttggccca	1020
47 ggaggtgtct acgctagaga aagatcagat gtgctttgg ggacaatgat gtttattatc	1080
48 gggctgaata tgctattgg tcctaagaaa aacctgact tgcttctca aacaaaaaac	1140
49 agttctaaag tgctttcag aaagagtgaa aaatacatga aacttttctt gtggctgctt	1200
50 gtttgtgtgg gatttgtggg attaggacta cggcataaaag cctatgagag aaaactgggc	1260
51 aaagtggcac caaccaaaga ggtctctgct gccatctggc ctttcaggtt tggatatgac	1320
52 aatgaagggt ggtcttagtct agaaagatca gtcacccatc tcaatgaaac aggtgcagat	1380
53 ttcataacaa ttttggagag tgatgtttctt aagccctata tggggaaacaa tgacttaacc	1440
54 atgtggctag gggaaaagtt gggtttctat acagactttg gtccaaagcac aaggatcac	1500
55 actggggga ttatggctt gtcagatc ccaattgtga aatctgagca tcacccctt	1560
56 ccgtcaccag agggcgagat cgaccacgac atcacattga cgttaacat ttcggcaag	1620
57 ctgggtgatt ttgtcgtgac acacttggg aaccacgaaatgacccatc cagggaaactg	1680
58 caggctattt ctgtttcaaa actactgaaa agtagctcta atcaagtat atttctggaa	1740

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59	tatatactt	cagcacctgg	ctccagagat	tatctacagc	tcactgaaca	tggcaatgtg	1800									
60	aaggatatcg	acagcaactga	tcatgacaga	tggtgtgaat	acattatgtt	tcgagggctg	1860									
61	atcaggttgg	gttatgcaag	aatctccat	gctgaactga	gtgattcaga	aattcagatg	1920									
62	gcaaaattta	ggatccctga	tgaccccact	aattatacg	acaaccaga	agtggtcata	1980									
63	gaccacagag	aagtttctga	gaaaattcat	tttaatccca	gatttggatc	ctacaaagaa	2040									
64	ggacacaatt	atgaaaacaa	ccatcatttt	catatgaata	ctcccaaata	cttttatga	2100									
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69	<212>	TYPE:	PRT													
70	<213>	ORGANISM:	Homo sapiens													
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74	1							5				10				15
75	Val	Ser	Trp	Ser	Leu	Tyr	His	Asp	Leu	Gly	Pro	Met	Ile	Tyr	Tyr	Phe
76								20				25				30
77	Pro	Leu	Gln	Thr	Leu	Glu	Leu	Thr	Gly	Leu	Glu	Gly	Phe	Ser	Ile	Ala
78								35				40				45
79	Phe	Leu	Ser	Pro	Ile	Phe	Leu	Thr	Ile	Thr	Pro	Phe	Trp	Lys	Leu	Val
80								50				55				60
81	Asn	Lys	Lys	Trp	Met	Leu	Thr	Leu	Leu	Arg	Ile	Ile	Thr	Ile	Gly	Ser
82	65							70				75				80
83	Ile	Ala	Ser	Phe	Gln	Ala	Pro	Asn	Ala	Lys	Leu	Arg	Leu	Met	Val	Leu
84								85				90				95
85	Ala	Leu	Gly	Val	Ser	Ser	Ser	Leu	Ile	Val	Gln	Ala	Val	Thr	Trp	Trp
86								100				105				110
87	Ser	Gly	Ser	His	Leu	Gln	Arg	Tyr	Leu	Arg	Ile	Trp	Gly	Phe	Ile	Leu
88								115				120				125
89	Gly	Gln	Ile	Val	Leu	Val	Val	Leu	Arg	Ile	Trp	Tyr	Thr	Ser	Leu	Asn
90								130				135				140
91	Pro	Ile	Trp	Ser	Tyr	Gln	Met	Ser	Asn	Lys	Val	Ile	Leu	Thr	Leu	Ser
92	145							145				150				160
93	Ala	Ile	Ala	Thr	Leu	Asp	Arg	Ile	Gly	Thr	Asp	Gly	Asp	Cys	Ser	Lys
94								165				170				175
95	Pro	Glu	Glu	Lys	Lys	Thr	Gly	Glu	Val	Ala	Thr	Gly	Met	Ala	Ser	Arg
96								180				185				190
97	Pro	Asn	Trp	Leu	Leu	Ala	Gly	Ala	Ala	Phe	Gly	Ser	Leu	Val	Phe	Leu
98								195				200				205
99	Thr	His	Trp	Val	Phe	Gly	Glu	Val	Ser	Leu	Val	Ser	Arg	Trp	Ala	Val
100								210				215				220
101	Ser	Gly	His	Pro	His	Pro	Gly	Pro	Asp	Pro	Asn	Pro	Phe	Gly	Ala	
102	225							225				230				240
103	Val	Leu	Leu	Cys	Leu	Ala	Ser	Gly	Leu	Met	Leu	Pro	Ser	Cys	Leu	Trp
104								245				250				255
105	Phe	Arg	Gly	Thr	Gly	Leu	Ile	Trp	Trp	Val	Thr	Gly	Thr	Ala	Ser	Ala
106								260				265				270
107	Ala	Gly	Leu	Leu	Tyr	Leu	His	Thr	Trp	Ala	Ala	Ala	Val	Ser	Gly	Cys
108								275				280				285
109	Val	Phe	Ala	Ile	Phe	Thr	Ala	Ser	Met	Trp	Pro	Gln	Thr	Leu	Gly	His

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110	290	295	300
111	Leu Ile Asn Ser Gly Thr Asn Pro Gly Lys Thr Met Thr Ile Ala Met		
112	305	310	315
113	Ile Phe Tyr Leu Leu Glu Ile Phe Phe Cys Ala Trp Cys Thr Ala Phe		320
114	325	330	335
115	Lys Phe Val Pro Gly Gly Val Tyr Ala Arg Glu Arg Ser Asp Val Leu		
116	340	345	350
117	Leu Gly Thr Met Met Leu Ile Ile Gly Leu Asn Met Leu Phe Gly Pro		
118	355	360	365
119	Lys Lys Asn Leu Asp Leu Leu Leu Gln Thr Lys Asn Ser Ser Lys Val		
120	370	375	380
121	Leu Phe Arg Lys Ser Glu Lys Tyr Met Lys Leu Phe Leu Trp Leu Leu		
122	385	390	395
123	400	405	410
124	Val Gly Val Gly Leu Leu Gly Leu Gly Leu Arg His Lys Ala Tyr Glu		415
125	Arg Lys Leu Gly Lys Val Ala Pro Thr Lys Glu Val Ser Ala Ala Ile		
126	420	425	430
127	Trp Pro Phe Arg Phe Gly Tyr Asp Asn Glu Gly Trp Ser Ser Leu Glu		
128	435	440	445
129	Arg Ser Ala His Leu Leu Asn Glu Thr Gly Ala Asp Phe Ile Thr Ile		
130	450	455	460
131	Leu Glu Ser Asp Ala Ser Lys Pro Tyr Met Gly Asn Asn Asp Leu Thr		
132	465	470	475
133	480	485	490
134	495	500	505
135	510	515	520
136	525	530	535
137	540	545	550
138	555	560	565
139	570	575	580
140	585	590	595
141	600	605	610
142	615	620	625
143	630	635	640
144	645	650	655
145	660	665	670
146	675	680	685

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159 His Phe His Met Asn Thr Pro Lys Tyr Phe Leu
160 690 695
162 <210> SEQ ID NO: 3
163 <211> LENGTH: 287
164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 3
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169 gagccaggta ctgaagtgtat atatcccaga aatatcactt gatttagagct acttttcagt 120
170 agttttgaaa cagcaatacg c tgcagttc ctgtcgaggt catcttcgtg gttccaaag 180
171 tgtgtcacga caaaaatccac cagcttgccc gaaatgttaa cggtcaatgt gatggcttgt 240
172 gcatcttgc tgtgtggcc aggctggctt caacgtgcag atagatc 287
174 <210> SEQ ID NO: 4
175 <211> LENGTH: 699
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
179 <400> SEQUENCE: 4
180 Met Thr Ser Leu Trp Arg Glu Ile Leu Leu Glu Ser Leu Leu Gly Cys
181 1 5 10 15
182 Val Ser Trp Ser Leu Tyr His Asp Leu Gly Pro Met Ile Tyr Tyr Phe
183 20 25 30
184 Pro Leu Gln Thr Leu Glu Leu Thr Gly Leu Glu Gly Phe Ser Ile Ala
185 35 40 45
186 Phe Leu Ser Pro Ile Phe Leu Thr Ile Thr Pro Phe Trp Lys Leu Val
187 50 55 60
188 Asn Lys Lys Trp Met Leu Thr Leu Leu Arg Ile Ile Thr Ile Gly Ser
189 65 70 75 80
190 Ile Ala Ser Phe Gln Ala Pro Asn Ala Lys Leu Arg Leu Met Val Leu
191 85 90 95
192 Ala Leu Gly Val Ser Ser Ser Leu Ile Val Gln Ala Val Thr Trp Trp
193 100 105 110
194 Ser Gly Ser His Leu Gln Arg Tyr Leu Arg Ile Trp Gly Phe Ile Leu
195 115 120 125
196 Gly Gln Ile Val Leu Val Val Leu Arg Ile Trp Tyr Thr Ser Leu Asn
197 130 135 140
198 Pro Ile Trp Ser Tyr Gln Met Ser Asn Lys Val Ile Leu Thr Leu Ser
199 145 150 155 160
200 Ala Ile Ala Thr Leu Asp Arg Ile Gly Thr Asp Gly Asp Cys Ser Lys
201 165 170 175
202 Pro Glu Glu Lys Lys Thr Gly Glu Val Ala Thr Gly Met Ala Ser Arg
203 180 185 190
204 Pro Asn Trp Leu Leu Ala Gly Ala Ala Phe Gly Ser Leu Val Phe Leu
205 195 200 205
206 Thr His Trp Val Phe Gly Glu Val Ser Leu Val Ser Arg Trp Ala Val
207 210 215 220
208 Ser Gly His Pro His Pro Gly Pro Asp Pro Asn Pro Phe Gly Gly Ala
209 225 230 235 240
210 Val Leu Leu Cys Leu Ala Ser Gly Leu Met Leu Pro Ser Cys Leu Trp
211 245 250 255

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212 Phe Arg Gly Thr Gly Leu Ile Trp Trp Val Thr Gly Thr Ala Ser Ala
213 260 265 270
214 Ala Gly Leu Leu Tyr Leu His Thr Trp Ala Ala Ala Val Ser Gly Cys
215 275 280 285
216 Val Phe Ala Ile Phe Thr Ala Ser Met Trp Pro Gln Thr Leu Gly His
217 290 295 300
218 Leu Ile Asn Ser Gly Thr Asn Pro Gly Lys Thr Met Thr Ile Ala Met
219 305 310 315 320
220 Ile Phe Tyr Leu Leu Glu Ile Phe Phe Cys Ala Trp Cys Thr Ala Phe
221 325 330 335
222 Lys Phe Val Pro Gly Gly Val Tyr Ala Arg Glu Arg Ser Asp Val Leu
223 340 345 350
224 Leu Gly Thr Met Met Leu Ile Ile Gly Leu Asn Met Leu Phe Gly Pro
225 355 360 365
226 Lys Lys Asn Leu Asp Leu Leu Gln Thr Lys Asn Ser Ser Lys Val
227 370 375 380
228 Leu Phe Arg Lys Ser Glu Lys Tyr Met Lys Leu Phe Leu Trp Leu Leu
229 385 390 395 400
230 Val Gly Val Gly Leu Leu Gly Leu Gly Leu Arg His Lys Ala Tyr Glu
231 405 410 415
232 Arg Lys Leu Gly Lys Val Ala Pro Thr Lys Glu Val Ser Ala Ala Ile
233 420 425 430
234 Trp Pro Phe Arg Phe Gly Tyr Asp Asn Glu Gly Trp Ser Ser Leu Glu
235 435 440 445
236 Arg Ser Ala His Leu Leu Asn Glu Thr Gly Ala Asp Phe Ile Thr Ile
237 450 455 460
238 Leu Glu Ser Asp Ala Ser Lys Pro Tyr Met Gly Asn Asn Asp Leu Thr
239 465 470 475 480
240 Met Trp Leu Gly Glu Lys Leu Gly Phe Tyr Thr Asp Phe Gly Pro Ser
241 485 490 495
242 Thr Arg Tyr His Thr Trp Gly Ile Met Ala Leu Ser Arg Tyr Pro Ile
243 500 505 510
244 Val Lys Ser Glu His His Leu Leu Pro Ser Pro Glu Gly Glu Ile Ala
245 515 520 525
246 Pro Ala Ile Thr Leu Thr Val Asn Ile Ser Gly Lys Leu Val Asp Phe
247 530 535 540
248 Val Val Thr His Phe Gly Asn His Glu Asp Asp Leu Asp Arg Lys Leu
249 545 550 555 560
250 Gln Ala Ile Ala Val Ser Lys Leu Leu Lys Ser Ser Ser Asn Gln Val
251 565 570 575
252 Ile Phe Leu Gly Tyr Ile Thr Ser Ala Pro Gly Ser Arg Asp Tyr Leu
253 580 585 590
254 Gln Leu Thr Glu His Gly Asn Val Lys Asp Ile Asp Ser Thr Asp His
255 595 600 605
256 Asp Arg Trp Cys Glu Tyr Ile Met Tyr Arg Gly Leu Ile Arg Leu Gly
257 610 615 620
258 Tyr Ala Arg Ile Ser His Ala Glu Leu Ser Asp Ser Glu Ile Gln Met
259 625 630 635 640
260 Ala Lys Phe Arg Ile Pro Asp Asp Pro Thr Asn Tyr Arg Asp Asn Gln

VERIFICATION SUMMARY

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